



OIPÉ

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/085,108

DATE: 03/13/2002

TIME: 10:18:02

Input Set : N:\Crf3\RULE60\10085108.raw

Output Set: N:\CRF3\03132002\J085108.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry

3 (ii) TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING

4 FOR

5 TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE

MAGE-C AND

6 MAGE-B FAMILIES AND USES THEREOF

7 (iii) NUMBER OF SEQUENCES: 26

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: Fulbright &amp; Jaworski L.L.P.

10 (B) STREET: 666 Fifth Avenue

11 (C) CITY: New York City

12 (D) STATE: New York

13 (E) COUNTRY: USA

14 (F) ZIP: 10103

15 (v) COMPUTER READABLE FORM:

16 (A) MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

17 (B) COMPUTER: IBM PS/2

18 (C) OPERATING SYSTEM: PC-DOS

19 (D) SOFTWARE: Wordperfect

20 (vi) CURRENT APPLICATION DATA:

C--&gt; 21 (A) APPLICATION NUMBER: US/10/085,108

C--&gt; 22 (B) FILING DATE: 01-Mar-2002

23 (C) CLASSIFICATION:

24 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: 09/501,104

26 (B) FILING DATE: 09-Feb-2000

27 (A) APPLICATION NUMBER: 09/468,433

28 (B) FILING DATE: December 17, 1999

29 (A) APPLICATION NUMBER: 09/066,281

30 (B) FILING DATE: April 24, 1998

31 (A) APPLICATION NUMBER: 08/845,528

32 (B) FILING DATE: April 25, 1997

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Mary Anne Schofield

35 (B) REGISTRATION NUMBER: 36,669

36 (C) REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: (212) 318-3100

39 (B) TELEFAX: (212) 318-3400

40 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:

42 (A) LENGTH: 4031 base pairs

ENTERED

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```

43      (B) TYPE: nucleic acid
44      (C) STRANDEDNESS: double-stranded
45      (D) TOPOLOGY: linear
46      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
47      GGATCGTCTC AGGTCAGCGG AGGGAGGAGA CTTATAGACC TATCCAGTCT TCAAGGTGCT 60
48      CCAGAAAGCA GGAGTTGAAG ACCTGGGTGT GAGGGACACA TACATCCTAA AAGCACCACA 120
49      GCAGAGGAGG CCCAGGCAGT GCCAGGAGTC AAGGTTCCCA GAAGACAAAC CCCCTAGGAA 180
50      GACAGGCGAC CTGTGAGGCC CTAGAGCACC ACCTTAAGAG AAGAAGAGCT GTAAGCCGGC 240
51      CTTTGTTCAGA GCCATCATGG GGGACAAGGA TATGCCTACT GCTGGGATGC CGAGTCTTCT 300
52      CCAGAGTTCC TCTGAGAGTC CTCAGAGTTG TCCTGAGGGG GAGGACTCCC AGTCTCCTCT 360
53      CCAGATTCCC CAGAGTTCTC CTGAGAGCGA CGACACCCTG TATCCTCTCC AGAGTCCTCA 420
54      GAGTCGTTCT GAGGGGGAGG ACTCCTCGGA TCCTCTCCAG AGACCTCCTG AGGGGAAGGA 480
55      CTCCCAGTCT CCTCTCCAGA TTCCCCAGAG TTCTCCTGAG GCGACGACA CCCAGTCTCC 540
56      TCTCCAGAA TCTCAGAGTT CTCCTGAGGG GAAGGACTCC CTGTCTCCTC TAGAGATTTC 600
57      TCAGAGCCCT CCTGAGGGTG AGGATGTCCA GTCTCCTCTG CAGAATCCTG CGAGTTCCTT 660
58      CTTCTCCTCT GCTTTATTGA GTATTTTCCA GAGTTCCCCT GAGAGAACTC AGAGTACTTT 720
59      TGAGGGTTTT CCCAGTCTC CTCTCCAGAT TCCTGTGAGC TCCTCCTCCT CCTCCACTTT 780
60      ATTGAGTCTT TTCCAGAGTT CCCCTGAGAG AACTCAGAGT ACTTTTGAGG GTTTTCCCA 840
61      GTCTCTTCTC CAGATTCTTA TGACCTCCTC CTTCTCCTCT ACTTTATTGA GTATTTTCCA 900
62      GAGTTCTCCT GAGAGTGCTC AAAGTACTTT TGAGGGTTTT CCCAGTCTC CTCTCCAGAT 960
63      TCCTGGGAGC CCCTCCTTCT CCTCCACTTT ACTGAGTCTT TTCCAGAGTT CCCCTGAGAG 1020
64      AACTCACAGT ACTTTTGAGG GTTTTCCCA GTCTCCTCTC CAGATTCTTA TGACCTCCTC 1080
65      CTTCTCCTCT ACTTTATTGA GTATTTTCCA GAGTTCTCCT GAGAGTGCTC AAAGTACTTT 1140
66      TGAGGGTTTT CCCAGTCTC CTCTCCAGAT TCCTGGGAGC CCCTCCTTCT CCTCCACTTT 1200
67      ACTGAGTCTT TTCCAGAGTT CCCCTGAGAG AACTCACAGT ACTTTTGAGG GTTTTCCCA 1260
68      GTCTCCTCTC CAGATTCTTA TGACCTCCTC CTTCTCCTCT ACTTTATTGA GTATTTTACA 1320
69      GAGTTCTCCT GAGAGTGCTC AAAGTGCTTT TGAGGGTTTT CCCAGTCTC CTCTCCAGAT 1380
70      TCCTGTGAGC TCCTCTTTCT CCTACACTTT ATTGAGTCTT TTCCAGAGTT CCCCTGAGAG 1440
71      AACTCAGAGT ACTTTTGAGG GTTTTCCCA GTCTCCTCTC CAGATTCTTG TGAGCTCCTC 1500
72      CTCCTCCTCC TCCACTTTAT TGAGTCTTTT CCAGAGTTCC CCTGAGTGTA CTCAAAGTAC 1560
73      TTTTGAGGGT TTTCCCCAGT CTCCTCTCCA GATTCCTCAG AGTCTCCTG AAGGGGAGAA 1620
74      TACCACTTCT CCTCTCCAGA TTGTTCCAAG TCTTCCTGAG TGGGAGGACT CCCTGTCTCC 1680
75      TCACTACTTT CCTCAGAGCC CTCCTCAGGG GGAGGACTCC CTATCTCCTC ACTACTTTCC 1740
76      TCAGAGCCCT CCTCAGGGGG AGGACTCCCT GTCTCCTCAC TACTTCTCTC AGAGCCCTCA 1800
77      GGGGGAGGAC TCCCTGTCTC CTCACTACTT TCCTCAGAGC CCTCCTCAGG GGGAGGACTC 1860
78      CATGTCTCCT CTCTACTTTT CTCAGAGTCC TCTTCAGGGG GAGGAATTCC AGTCTTCTCT 1920
79      CCAGAGCCCT GTGAGCATCT GTCCTCCTC CACTCCATCC AGTCTTCCCC AGAGTTTCCC 1980
80      TGAGAGTTCT CAGAGTCCTC CTGAGGGGCC TGTCCAGTCT CCTCTCCATA GTCCTCAGAG 2040
81      CCCTCCTGAG GGGATGCACT CCCAATCTCC TCTCCAGAGT CCTGAGAGTG CTCCTGAGGG 2100
82      GGAGGATTCC CTGTCTCCTC TCCAAATTCC TCAGAGTCTT CTTGAGGGAG AGGACTCCCT 2160
83      GTCTTCTCTC CATTTTCTCT AGAGTCTCTC TGAGTGGGAG GACTCCCTCT CTCCTCTCCA 2220
84      CTTTCTCAG TTTCTCCTC AGGGGGAGGA CTTCAGTCT TCTCTCCAGA GTCCTGTGAG 2280
85      TATCTGCTCC TCCTCCACTT CTTTGAGTCT TCCCAGAGT TTCCCTGAGA GTCCTCAGAG 2340
86      TCCTCCTGAG GGGCCTGCTC AGTCTCCTT CCAGAGACCT GTCAGTCTCT TCTTCTCCTA 2400
87      CACTTTAGCG AGTCTTCTCC AAAGTTCCCA TGAGAGTCTT CAGAGTCTCT CTCGAGGGCC 2460
88      TGCCCAGTCT CCTCTCCAGA GTCCTGTGAG CTCCTTCCCC TCCTCCACTT CATCGAGTCT 2520
89      TTCCCAGAGT TCTCCTGTGA GTCCTTCCC CTCCTCCACT TCATCGAGTC TTTCCAAGAG 2580
90      TTCCCCTGAG AGTCTCTCTC AGAGTCTCTG GATCTCCTTC TCCTCCTCCA CTTATTGAG 2640
91      CCCATTGAGT GAAGAGTCCA GCAGCCCAGT AGATGAATAT ACAAGTTCCT CAGACACCTT 2700

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92  GCTAGAGAGT GATTCCCTGA CAGACAGCGA GTCCTTGATA GAGAGCGAGC CTTGTGTTAC 2760
93  TTATACACTG GATGAAAAGG TGGACGAGTT GGCGCGGTTT CTTCTCCTCA AATATCAAGT 2820
94  GAAGCAGCCT ATCACAAAGG CAGAGATGCT GACGAATGTC ATCAGCAGGT ACACGGGCTA 2880
95  CTTTCCTGTG ATCTTCAGGA AAGCCCGTGA GTTCATAGAG ATACTTTTTG GCATTTCCCT 2940
96  GAGAGAAGTG GACCCGTGATG ACTCCTATGT CTTTGTA AAC ACATTAGACC TCACCTCTGA 3000
97  GGGGTGTCTG AGTGATGAGC AGGGCATGTC CCAGAACCGC CTCCTGATTC TTATTCTGAG 3060
98  TATCATCTTC ATAAAGGGCA CCTATGCCTC TGAGGAGGTC ATCTGGGATG TGCTGAGTGG 3120
99  AATAGGGGTG CGTGCTGGGA GGGAGCACTT TGCCTTTGGG GAGCCCAGGG AGCTCCTCAC 3180
100 TAAAGTTTGG GTGCAGGAAC ATTACCTAGA GTACCGGGAG GTGCCCAACT CTTCTCCTCC 3240
101 TCGTTACGAA TTCCTGTGGG GTCCAAGAGC TCATTACAGAA GTCATTAAGA GGAAAGTAGT 3300
102 AGAGTTTTTG GCCATGCTAA AGAATACCGT CCTATTACC TTTCCATCCT CTTACAAGGA 3360
103 TGCTTTGAAA GATGTGGAAG AGAGAGCCCA GGCCATAATT GACACCACAG ATGATTCGAC 3420
104 TGCCACAGAA AGTGCAAGCT CCAGTGTCAT GTCCCCCAGC TTCTCTTCTG ATGGAAGTCT 3480
105 AGGGCAGATT CTTCCCTCTG AGTTTGAAGG GGGCAGTCGA GTTTCTACGT GGTGAGGGC 3540
106 CTGGTTGAGG CTGGAGAGAA CACAGTGCTA TTTGCATTTT TGTTCCATAT GGGTAGTTAT 3600
107 GGGGTTTACC TGTTTTACTT TTGGGTATTT TTCAAATGCT TTTCTTATTA ATAACAGGTT 3660
108 TAAATAGCTT CAGAATCCTA GTTTATGCAC ATGAGTCGCA CATGTATTGC TGTTTTTCTG 3720
109 GTTTAAGAGT AACAGTTTGA TATTTTGTA AAACAAAAC ACACCCAAAC ACACCACATT 3780
110 GGGAAAACCT TCTGCCTCAT TTTGTGATGT GTCACAGGTT AATGTGGTGT TACTGTAGGA 3840
111 ATTTTCTTGA AACTGTGAAG GAACTCTGCA GTTAAATAGT GGAATAAAGT AAAGGATTGT 3900
112 TAATGTTTGC ATTTCTCAG GTCCTTTAGT CTGTTGTTCT TGAAACTAA AGATACATAC 3960
113 CTGGTTTGCT TGGCTTACGT AAGAAAGTAG AAGAAAGTAA ACTGTAATAA ATAAAAAAA 4020
114 AAAAAAAAAA A 4031

116 (2) INFORMATION FOR SEQ ID NO: 2:
117 (i) SEQUENCE CHARACTERISTICS:
118 (A) LENGTH: 12 base pairs
119 (B) TYPE: nucleic acid
120 (C) STRANDEDNESS: single-stranded
121 (D) TOPOLOGY: linear
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
123 GATCTGCGGT GA 12
125 (2) INFORMATION FOR SEQ ID NO: 3:
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 12 base pairs
128 (B) TYPE: nucleic acid
129 (C) STRANDEDNESS: SINGLE-stranded
130 (D) TOPOLOGY: linear
131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
132 GATCTGTTCA TG 12
134 (2) INFORMATION FOR SEQ ID NO: 4:
135 (i) SEQUENCE CHARACTERISTICS:
136 (A) LENGTH: 12 base pairs
137 (B) TYPE: nucleic acid
138 (C) STRANDEDNESS: single-stranded
139 (D) TOPOLOGY: linear
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
141 GATCTTCCCT CG 12
143 (2) INFORMATION FOR SEQ ID NO: 5:
144 (i) SEQUENCE CHARACTERISTICS:

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Input Set : N:\Crf3\RULE60\10085108.raw

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145         (A) LENGTH: 46 base pairs
146         (B) TYPE: nucleic acid
147         (C) STRANDEDNESS: single-stranded
148         (D) TOPOLOGY: linear
149     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
150     NAACTGGAAG AATTCGCGGC CGCAGGAATT TTTTTTTTTT TTTTTT      46
152 (2) INFORMATION FOR SEQ ID NO: 6:
153     (i) SEQUENCE CHARACTERISTICS:
154         (A) LENGTH: 12 base pairs
155         (B) TYPE: nucleic acid
156         (C) STRANDEDNESS: single-stranded
157         (D) TOPOLOGY: linear
158     (ix) FEATURE:
159         (D) OTHER INFORMATION: BstX1 adapter upper strand
160     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
161     CTTTCCAGCA CA      12
163 (2) INFORMATION FOR SEQ ID NO: 7:
164     (i) SEQUENCE CHARACTERISTICS:
165         (A) LENGTH: 1142
166         (B) TYPE: amino acids
167         (C) STRANDEDNESS: single-stranded
168         (D) TOPOLOGY: linear
169     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
170     Met Gly Asp Lys Asp Met Pro Thr Ala Gly Met Pro Ser Leu Leu Gln
171           5              10              15
172     Ser Ser Ser Glu Ser Pro Gln Ser Cys Pro Glu Gly Glu Asp Ser Gln
173           20              25              30
174     Ser Pro Leu Gln Ile Pro Gln Ser Ser Pro Glu Ser Asp Thr Leu
175           35              40              45
176     Tyr Pro Leu Gln Ser Pro Gln Ser Arg Ser Glu Gly Glu Asp Ser Ser
177           50              55              60
178     Asp Pro Leu Gln Arg Pro Pro Glu Gly Lys Asp Ser Gln Ser Pro Leu
179           65              70              75              80
180     Gln Ile Pro Gln Ser Ser Pro Glu Gly Asp Asp Thr Gln Ser Pro Leu
181           85              90              95
182     Gln Asn Ser Gln Ser Ser Pro Glu Gly Lys Asp Ser Leu Ser Pro Leu
183           100             105             110
184     Glu Ile Ser Gln Ser Pro Pro Glu Gly Glu Asp Val Gln Ser Pro Leu
185           115             120             125
186     Gln Asn Pro Ala Ser Ser Phe Ser Ser Ala Leu Leu Ser Ile Phe
187           130             135             140
188     Gln Ser Ser Pro Glu Ser Ile Gln Ser Pro Phe Glu Gly Phe Pro Gln
189           145             150             155             160
190     Ser Val Leu Gln Ile Pro Val Ser Ala Ala Ser Ser Ser Thr Leu Val
191           165             170             175
192     Ser Ile Phe Gln Ser Ser Pro Glu Ser Thr Gln Ser Pro Phe Glu Gly
193           180             185             190
194     Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser Arg Ser Phe Ser Ser
195           195             200             205

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```

196   Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro Glu Arg Ser Gln Arg Thr
197       210               215               220
198   Ser Glu Gly Phe Ala Gln Ser Pro Leu Gln Ile Pro Val Ser Ser Ser
199       225               230               235               240
200   Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr
201       245               250               255
202   Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Val
203       260               265               270
204   Ser Arg Ser Phe Ser Ser Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro
205       275               280               285
206   Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Ala Gln Ser Pro Leu Gln
207       290               295               300
208   Ile Pro Val Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln
209       305               310               315               320
210   Ser Ser Pro Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser
211       325               330               335
212   Leu Leu Gln Ile Pro Met Thr Ser Ser Phe Ser Ser Thr Leu Leu Ser
213       340               345               350
214   Ile Phe Gln Ser Ser Pro Glu Ser Ala Gln Ser Thr Phe Glu Gly Phe
215       355               360               365
216   Pro Gln Ser Pro Leu Gln Ile Pro Gly Ser Pro Ser Phe Ser Ser Thr
217       370               375               380
218   Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr His Ser Thr Phe
219       385               390               395               400
220   Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Met Thr Ser Ser Phe
221       405               410               415
222   Ser Ser Thr Leu Leu Ser Ile Leu Gln Ser Ser Pro Glu Ser Ala Gln
223       420               425               430
224   Ser Ala Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser
225       435               440               445
226   Ser Ser Phe Ser Tyr Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu
227       450               455               460
228   Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile
229       465               470               475               480
230   Pro Val Ser Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln
231       485               490               495
232   Ser Ser Pro Glu Cys Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser
233       500               505               510
234   Pro Leu Gln Ile Pro Gln Ser Pro Pro Glu Gly Glu Asn Thr His Ser
235       515               520               525
236   Pro Leu Gln Ile Val Pro Ser Leu Pro Glu Trp Glu Asp Ser Leu Ser
237       530               535               540
238   Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser
239       545               550               555               560
240   Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser
241       565               570               575
242   Pro His Tyr Phe Pro Gln Ser Pro Gln Gly Glu Asp Ser Leu Ser Pro
243       580               585               590
244   His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Met Ser Pro

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/085,108

DATE: 03/13/2002  
TIME: 10:18:03

Input Set : N:\Crf3\RULE60\10085108.raw  
Output Set: N:\CRF3\03132002\J085108.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/085,108

DATE: 03/13/2002

TIME: 10:18:03

Input Set : N:\Crf3\RULE60\10085108.raw

Output Set: N:\CRF3\03132002\J085108.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]